



05030301

FIG. 1A

V F H S V G N L E T L I L D S N P L A C	367
GTG TTC CAC TCG GTG GGC AAC CTG GAG ACA CTC ATC CTG GAC TCC AAC CCG CTG GCG TCC	1231
D C R L L W V F R R R W R L N F N R Q Q	387
GAC TGT CCG CTC CTG TCG GTG TTC CCG CCG CCG TCG CCG CTC AAC TTC AAC CCG CAG CAG	1291
P T C A T P E F V Q G K E F K D F P D V	407
CCC ACG TCC GCG ACG CCC GAG TTT CTC CAG GGC AAG GAG TTC AAG GAC TTC CCT GAT GTG	1351
L L P N Y F T C R R A R I R D R K A Q Q	427
CTA CTG CCC AAC TAC TTC ACC TCC CCG CCG GCG CCG ATC CCG GAC CCG AAG GCG CAG CAG	1411
V F V D E G H T V Q F V C R A D G D P P	447
GTG TTT GTG GAC GAG GGC CAC ACG GTG CAG TTT GTG TCC CCG GCG GAT GGC GAC CCG CCG	1471
P A I L W L S P R K H L V S A K S N G R	467
CCC GCG ATC CTC TCG CTC TCA CCC CGA AAG CAC CTG GTC TCA GCG AAG AGC AAT GCG CCG	1531
L T V F P D G T L E V R Y A Q V Q D N G	487
CTC ACA GTC TTC CCT GAT GGC ACG CTG GAG GTG CCG TAC GCG CAG GTA CAG GAC AAC GCG	1591
T Y L C I A A N A G G N D S M P A H L H	507
ACG TAC CTG TCC ATC CCG GCG AAC GCG GCG GCG AAC GAC TCC ATG CCC GCG CAC CTG CAT	1651
V R S Y S P D W P H Q P N K T F A F I S	527
GTG CCG ACG TAC TCG CCC GAC TCG CCC CAT CAG CCC AAC AAG ACC TTC GGT TTC ATC TCC	1711
N Q P G E G E A N S T R A T V P F P F D	547
AAC CAG CCG GCG GAG GGA GAG GCG AAC AGC ACC CCG GCG ACT GTG CCT TTC CCC TTC GAC	1771
I K T L I I A T T M G F I S F L G V V L	567
ATC AAG ACC CTC ATC ATC GCG ACC ACC ATG GCG TTC ATC TCT TTC CTG GCG GTC GTC CTC	1831
F C L V L L F L W S R G K G N T K H N I	587
TTC TCC CTG GTG CTG CTG TTT CTC TCG AGC CCG GCG AAG GCG AAC ACA AAG CAC AAC ATC	1891
E I E Y V P R K S D A G I S S A D A P R	607
GAG ATC GAG TAT GTG CCC CGA AAG TCG GAC CGA GCG ATC AGC TCC GCG GAC GCG CCC CCG	1951
K F N M K M I *	615
AAG TTC AAC ATG AAG ATG ATA TGA	1975
GGCCCGGGCGGGGGGGCAGGGACCCCCCGGGGGGGGGGGCAGGGGAAGGGGGCTGGCCCGCCACCTGCTCACTCTCCAGTCC	2054
TTCACCTCTCTGCTTACCTTTCTACACAGCTTCTCTTTCTCTCCCTTCCCGCTTGGTCCCTGCTGCGGGGGGGCAGCC	2133
CTCACCACTTGGCTTCTTCTTACCAAGGAAGCTCAGAAGCCCGAGACCTGGGGACCCCACTTACACAGGGGCATTGACAGAC	2212
TGGAGTTTAAGCGGACGAGCCGACCGGGCAGAGTCAATAATTCAATAAAAAAGTTACGAACCTTTCTCTGTAACCTG	2291
GGTTTCAATAATTATGGATTTTATGAAAAGTTGAATAATAAAAAAAAAAAAAAAAAAAG	2351

FIG. 1B

																		M	A	G	S	P	
GAATTCGGCAGGAGGCCGACCGCATTCGGCCGCG/MCGRRGCCCGCGCTGCTGCTGGGGCAGC	ATG	GCG	GGG	TGG	CCG														5				
L L W G :P R A G G V G L L V L L L L G L	25																						
CTG CTC TGG GGG CCG CCG GCC GGG GGC CTC GGC CTT TTG GTG CTG CTG CTG CTC GGC CTG	132																						
F R P P P A L C A R P V K E P R G L S A	45																						
TTT CCG CCG CCC CCC GCG CTC TGC GCG CCG CCG GTA AAG GAG CCC CCG GGC CTA AGC GCA	132																						
A S P P L A E T G A P R R F R R S V P R	65																						
GGG TCT CCG CCC TTG GCT GAG ACT GGC GCT CTT GGC CCC TTC CCG CCG TCA GTG CCC CGA	252																						
G E A A G A V Q E L A R A L A H L L E A	95																						
GGT GAG GCG GCG GCG GCG GTG CAG GAG CTG GCG CCG GCG CTG GCG CAT CTG CTG GAG GGC	312																						
E R Q E R A R A E A Q E A E D Q Q A R V	105																						
GAA CTT CAG GAG CCG GCG CCG GCC GAG CCG CAG GAG GCT GAG GAT CAG CAG GCG CCG GTC	372																						
L A Q L L R V W G A P R N S D P A L G L	125																						
CTG GCG CAG CTG CTG CCG CTC TGG GGC GCC CCC CCG AAC TCT GAT CCG GCT CTG GGC TTG	432																						
D D D P D A P A A Q L A R A L L R A R L	145																						
GAC GAC GAC CCC GAC GCG CTT GCA GCG CAG CTC GCT CCG GCT CTG CTC CCG GCC CCG CTT	492																						
D P A A L A A Q L V P A P V P A A A L R	165																						
GAC CTT GCC GGC CTA GCA GCC CAG CTT GTC CCC GCG CCC GTC CCC GGC GCG GCG CTC CGA	552																						
P R P P V Y D D G P A G P D A E E A G D	185																						
CCC CCG CCC CCG GTC TAC GAC GAC GGC CCC CCG GGC CCG GAT GCT GAG GAG GCA GGC GAC	612																						
E T P D V D P E L L R Y L L G R I L A G	205																						
GAG ACA CCC GAC GTG GAC CCC GAG CTG TTG AGG TAC TTG CTG GGA CCG ATT CTT CCG GGA	672																						
S A D S E G V A A P R R L R R A A D H D	225																						
AGC GCG GAC TCC GAG GCG GTG GCA GCC CCG CCG CCG CTC CCG CGT GGC GGC GAC CAC GAT	732																						
V G S E L P P E G V L G A L L R V K R L	245																						
GTG GGC TCT GAG CTG CCC CTT GAG GGC GTG CTG GCG GCG CTG CTG CGT GTG AAA CCG CTA	792																						
E T P A P Q V P A R R L L P P	261																						
GAG ACC CCG GCG CCC CAG GTG CTT GCA GCG CCG CTC TTG CCA CCC TGA	840																						
GCATCTGCCCCGATCCCTGTGCAACCTTGGGACCCCGAAGTCCCCCCCCCATCCCCCCACCAAGACTGCTCCCCCCCCAGCAC	919																						
GTCCAGAGCAACTTACCCCCCGGCAGCCAGCCCTCTCACCCGAGGATCCCTTACCCCCCTGGC	979																						

FIG. 2

Percent Similarity: 49.308 Percent Identity: 29.412

T79	1	MLAGGVRSMPSPLLACWQPILLVLGVSLSGS..ATGCPPRCECSAQDR.	47
		: : : : : : : : : : : : . . .	
D45913	1MARLSTGKAAC.QVVLGLLITSLTESSILTSEC?QLCVCEIRPWF	44
T79	48AVLCHRKRFVAVPEGIPTETRLDLGKNRIKTLNQDEFAS	87
		. : : : : : : : . .	
D45913	45	TPQSTYREATTVDCNDLRLTRIPGNLSSDTQVLLSQSNNI.....	84
T79	88	FPHLEELELNENIVSAVEPGAFNNLFLNRLTLGLRSNRLKLIPLGVFTGLS	137
		: : : : : : : :	
D45913	85AKTVDELQQLFNLTELDIFSQNNFTNIKEVGLANLT	119
T79	138	NLTKLDTRENNKIVILLDYMFDLYNLKSLEVGDNDLVYISHRAFSGLS	187
		. . . : : . . . : : .	
D45913	120	QLTTLHLEENQISEMTDYCLQDLSNLQELYINHNOISTISANAFSGLKNL	169
T79	188	EQLTLEKCNLTSTIPTALSHLHGLIVLRLRHLNINAIIRDYSFKRLYRLKV	237
		. : : . . : : : : : :	
D45913	170	LRLHLNSNKLKVIDSRWFDSTPNLEILMIGENPVIGILDMNFRPLSNLRS	219
T79	238	LEISHWPYLDTMTFNCYGLN.LTSLSITHCNLTAVPYLAVRHLVYLRFL	286
		: : . : . . : . . :	
D45913	220	LVLAG.MYLTDPGNALVGLDSLESLSFYDNKLIKVPQLALQKVPNLKFL	268
T79	287	NLSYNPISTIEGSMHELLRLQEIQLVG.GQLAVVEPY.....	323
		: . . : : : : : : : : . : . :	
D45913	269	DLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLPELTKLE	318
T79	324AFRGLNYLRVLNVSGNQLTTLEESVFHSGVGNLETIL	360
		: : : : . . . : : :	
D45913	319	ATNNPKLSYIHLAFRSVPALESMLNMLNAVYQKTVESLPNLREISI	368
T79	361	DSNPLACDCRLLWVFRWRRLNFRNQPT.CATPEFVQGKEFKDFPDVLL	409
		. : : . . : : . . . : : :	
D45913	369	HSNPLRCDCVIHWINSNKTNIREFMEPLSMFCAMPPEYRGQOVK...EVLI	415
T79	410	PNYFT.CRRARIRDRKAQOVFVDEGHTVQFVCRADGDPFPAILWLSPRKH	458
		. : . . : : : : : : : : . . : .	
D45913	416	QDSSEQCLPMISHDTFPNHLNMDIGTTLFLDCRAMAEPEPEIYVWTPIGN	465
T79	459	LVSAKS.NGRLTVPDGTLEVRYAQVQDNGTYLCIAANAGGNDSPHAHLH	507
		: . . . : : : : : : : : 	
D45913	466	KITVETLSDKYKLSSEGTLEIANIQIEDSGRYTCVAQNVQGADTRVATIK	515
T79	508	V.....RSYSPDWPHQ	518
		: : : :	
D45913	516	VNGTLLDGAQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDN	565
T79	519	PNKTF.....AFISNQPGEGEANSTRA	540

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FIG. 3A

205770" 03E030

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      |: |:                               . | .|....: .| |
D45913 566 PHITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVVTK 615
T79      541 T/PFPFDIKTLIIATTMGFI..SFLGVVLFCLVLLFLWSRGKGNTKHIE 588
      |.:|:|:|.. ..|:~: : |:~:|: :. : ~:~: .| | .. |:
D45913 616 TAAFALDISDHETSTALAAVMGSMFAVISLASIAIYIAKRFRKKNYHSL 665
T79      589 IEYVPRKSDAGISSADAPRKFNMKMI..... 614
      .|:~:~:|. ~:~: |. :|:~:
D45913 666 KKYMQKTSSIPLNEL.YPPLINLWEADSDKDKDGSADTKPTQVDTSRSYY 714

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FIG. 3B

205170" 685E0860

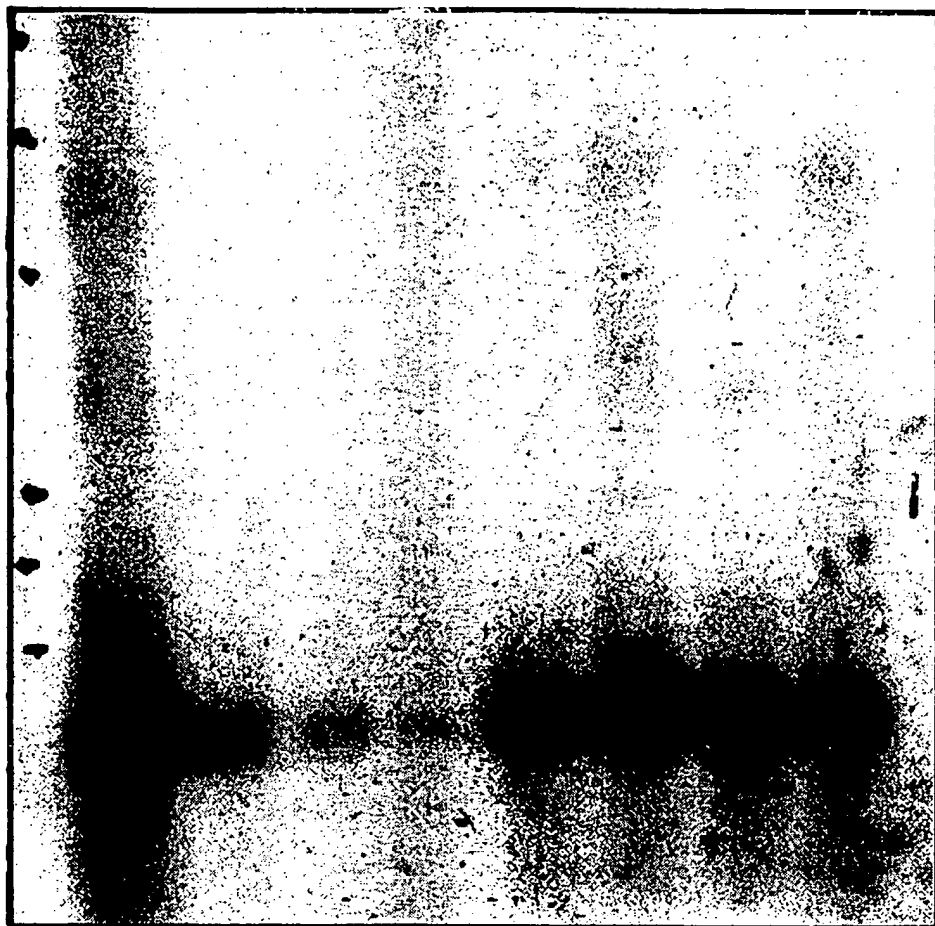


FIG. 4

T R P I L V I H D E Q K G P E V T S N	19
CC AGC CGT CCG ATC TTG GTC ATC CAC GAT GAA CAG AAG GGG CCG GAA GTG ACC TCC AAT	59
A A L T L R N F C N W Q K Q H N P P S D	39
GCT GCC CTC ACT CTG CCG AAC TTT TCC AAC TCG CAG AAG CAG CAC AAC CCA CCC AGT GAC	119
R D A E H Y D T A I L F T R Q D L C G S	59
CCG GAT GCA GAG CAC TAT GAC ACA GCA ATT CTT TTC ACC AGA CAG GAC TTG TGT GGG TCC	179
Q T C D T L G M A D V G T V C D P S R S	79
CAG ACA TGT GAT ACT CTT GGG ATG GCT GAT GTT GGA ACT GTG TGT GAT CCG AGC AGA AGC	239
C S V I E D D G L Q A A F T T A H E L G	99
TOC TCC GTC ATA GAA GAT GAT GGT TTA CAA GCT GCC TTC ACC ACA GCC CAT GAA TTA GGC	299
H V F N M P H D D A K Q C A S L N G V N	119
CAC GTG TTT AAC ATG CCA CAT GAT GAT GCA AAG CAG TGT GCC AGC CTT AAT GGT GTG AAC	359
Q D S H M M A S M L S N L D H S Q P W S	139
CAG GAT TCC CAC ATG ATG GCG TCA ATG CTT TCC AAC CTG GAC CAC AGC CAG CCT TCG TCT	419
P C S A Y M I T S F L D N G H G E C L M	159
CCT TCC AGT GCC TAC ATG ATT ACA TCA TTT CTG GAT AAT GGT CAT GGG GAA TGT TTG ATG	479
D K P Q N P I Q L P G D L P G T S Y D A	179
GAC AAG CCT CAG AAT CCC ATA CAG CTC CCA GGC GAT CTC CTT GGC ACC TCG TAC GAT GCC	539
N R Q C Q F T F G E D S K H C P D A A S	199
AAC CCG CAG TCC CAG TTT ACA TTT GGG GAG GAC TCC AAA CAC TCC CTT GAT GCA GCC AGC	599
T C S T L W C T G T S G G V L V C Q T K	219
ACA TGT AGC ACC TTG TCG TGT ACC GGC ACC TCT TGT GGG GTG CTG GTG TGT CAA ACC AAA	659
H F P W A D G T S C G E G K W C I N G K	239
CAC TTC CCG TCG GCG GAT GGC ACC AGC TGT GCA GAA GGG AAA TGG TGT ATC AAC GGC AAG	719
C V N K T D R K H F D T P F H G S W G M	259
TGT GTG AAC AAA ACC GAC AGA AAG CAT TTT GAT ACG CTT TTT CAT GGA AGC TCG GGA ATG	779
W G P W G D C S R T C G G G V Q Y T M R	279
TGG GGG CTT TCG GGA GAC TGT TCG AGA ACG TCC GGT GGA GGA GTC CAG TAC ACG ATG AGG	839
E C D N P V P K N G G K Y C E G K R V R	299
GAA TGT GAC AAC CCA GTC CCA AAG AAT GGA GGG AAG TAC TGT GAA GGC AAA CCA GTG CCG	999
Y R S C N L E D C P D N N G K T F R E E	319
TAC AGA TCC TGT AAC CTT GAG GAC TGT CCA GAC AAT AAT GGA AAA ACC TTT AGA GAG GAA	959
Q C E A H N E F S K A S F G S G P A V E	339
CAA TGT GAA GCA CAC AAC GAG TTT TCA AAA GCT TCC TTT GGG AGT GGG CTT GCG GTG GAA	1019
W I P K Y A G V S P K D R C K L I C Q A	359
TGG ATT CCC AAG TAC GCT GGC GTC TCA CCA AAG GAC AGG TCC AAG CTC ATC TCC CAA GCC	1079
K G I G Y F F V L Q P K V V D G T P C S	379
AAA GGC ATT GGC TAC TTC TTC GTT TTG CAG CCC AAG GTT GGA GAT GGT ACT CCA TGT AGC	1139

FIG. 5A

P D S T S V C V Q G Q C V K A G C D R I 399
 CCA GAT TCC ACC TCT GTC TOT GTG CAA GGA CAG TGT GTA AAA GGT GGT TOT GAT CCC ATC 1199

I D S K K K F D R C G V C G G N G S T C 419
 AEA GAC TCC AAA AAG AAG TTT GAT AAA TGT GGT GTT TCC GGG GGA AAT GGA TCT ACT TOT 1259

K K I S G S V T S A K P G Y H D I I T I 439
 AAA AAA AEA TCA GGA TCA GTT ACT AGT GCA AAA CCT GGA TAT CAT GAT ATC ATC ACA ATT 1319

P T G A T N I E V K Q R N Q R G S R N N 459
 CCA ACT GGA GCC ACC AAC ATC GAA GTG AAA CAG CCG AAC CAG AGG GGA TCC AGG AAC AAT 1379

G S F L A I K A A D G T Y I L N G D Y T 479
 GGC AGC TTT CTT GCC ATC AAA GCT GCT GAT GGC ACA TAT ATT CTT AAT GGT GAC TAC ACT 1439

L S T L E Q D I M Y K G V V L R Y S G S 499
 TTG TCC ACC TTA GAG CAA GAC ATT ATG TAC AAA GGT GTT GTC TTG AGG TAC AGC GGC TCC 1499

S A A L E R I R S F S P L K E P L T I Q 519
 TOT GCG GCA TTG GAA AGA ATT CCC AGC TTT AGC CCT CTC AAA GAG CCC TTG ACC ATC CAG 1559

V L T V G N A L R P K I K Y T Y F V K K 539
 GTT CTT ACT GTG GGC AAT GCC CTT GCA CCT AAA ATT AAA TAC ACC TAC TTT GEA AAG AAG 1619

K K E S F N A I P T F S A W V I E E W G 559
 AAG AAG GAA TCT TTC AAT GCT ATC CCC ACT TTT TCA GCA TGG GTC ATT GAA GAG TGG GGC 1679

E C S K T C G K G Y K K R S L K C L S H 579
 GAA TOT TCT AAG ACC TOT GGG AAG GGT TAC AAA AAA AGA AGC TTG AAG TOT CTG TCC CAT 1739

D G G V L S H E S C D P L K K P K H F I 599
 GAT GCA GGG GTG TTA TCT CAT GAG AGC TOT GAT CCT TTA AAG AAA CCT AAA CAT TTC ATA 1799

D F C T M A E C S * 609
 GAC TTT TGC ACA ATG GCA GAA TCC AGT TAA 1829

GTGGTTTAAAGTGGTGTGTTAGCTCTGAGGGCAAGGCAAGTGAGGAAGGGCTGGTCCAGGGAAAGCAAGAGGGCTGGAGGG 1908

ATCCAGGCTATCTTCCCACTAACCACTGAGGTGTATCAGTAAGGTGGGATTAAGGGGTAGATAGAAAAGGAGTTGAAT 1987

CATCAGAGTAAGTGGCAGTTGCAAAATTTCTAGGATAGTTAGTGAGGATTATTAAGCTCTGAGCACTGATATAGCATA 2066

ATAAGGCCCCGGGCATTATATATATATTTCTTTTGTACATCTATTAACAAGTTTAGAAAAACAAGCAATTGTCAA 2145

AAAAGTTAGAACTATTACAACCCCTGTTTCTCTGGTACTTATCAAAATACTTAGTATCATGGGGGTGGGAAATGAAAAGT 2224

AGGAGAAAAGTGAGATTCTTACTAAGACCTGTTTTACTTTACCTCACTAACAATGGGGGGAGAAAGGAGTACAAATAGGA 2303

TCTTTGACCGCACTGTTTTATGGCTGCTATGGTTTCAGAGAATGTTTTATACATTATTTCTACCGAGAATTAAACTTCA 2382

GATTGTTCAACATGAGAGAAAGGCTCAGCAAGCTGAATAACGCAAAATGGCTTCTCTTTCTCTTTTCTGGACCTCTCA 2461

GTCTTTATTTGTGTAATTCATTTTGAGGAAAAACAACCTCCATGTATTTATTCAGTGCAATTAAGTCTACAATGGAAA 2540

AAAAGCAGTGAGCATTAGATGCTGGTAAAAGCTAGAGGAGACACAATGAGCTTAGTACCTCCAAGCTTCTTTCTTTCT 2619

TACCATGTAAACCTGCTTTTGGGAATATGGATGTAAAGAGTAAGTTGTGTCTCATGAAAATCAGTACAATCACACAAGG 2698

FIG. 5B

AGGATGAAACGCGCGACAAAAATGAGGTGTGTAGACAGGTCCTCAGGTTTGGGACATTGAGATCACTTCTCTTC	2777
TGTTGGGAGGCTGCTGAGGGTAGCAGGTCTCTCTCAGGCTGCTCCACAGTCTATCTCTGGTGAATGCTCTCTC	2856
AGCTCTTCTCTGAGAAATATGATTTTTTCTCTATGTATATAGTAAATATGTTACTATTAATTACATGTACTTTATAGT	2935
ATTGCTTGGGTGTTCTCTCTCAGAAGGACTATAGTTAGTAATAAATGCCCTTAATAACATATTTATTTTATACATTT	3014
ATTCTAATGAAAAAACTTTTAAATTATATCGCTTTTCTGAGTGCATATAAAATAGAGTATTTATACAATATATGT	3093
TACTAGAAATAAAGAACACTTTTCTGAAAAAAGGGCGGGCGC	3147

FIG. 5C

251 DQSMADFHSGSLKHYLLTLFVVAARFYAHFSDRNSISLWVKILVYTEQ 300
||||:|
1TRPILVDEDEQ 11

301 KGFEVTSNAALTILRNFCNWKQHNPSDRDPFHYDTAILFTRQDLGGSHT 350
||||:|
12 KGFEVTSNAALTILRNFCNWKQHNPSDRDAEHYDTAILFTRQDLGGSQT 61

351 CDTLGMADVGTVCDFSRSCSVTEEDGLQAAFTTABELGHVFNMPHDDAKH 400
||||:|
62 CDTLGMADVGTVCDFSRSCSVTEEDGLQAAFTTABELGHVFNMPHDDAKQ 111

401 CASLNGVSGDSHLMASMLSSLCHSQFWSPCSAYMVTSPFLNGHGECILMK 450
||||:|
112 CASLNGVNGDSHLMASMLSNLCHSQFWSPCSAYMVTSPFLNGHGECILMK 161

451 PQNPICLPSDLPGTLVDANRQCQFTFGESKHCPCDAASTCTILNCTGTSG 500
||||:|
162 PQNPICLPDGLPGTLYDANRQCQFTFGESKHCPCDAASTCTILNCTGTSG 211

501 GLLVCQTHFPWADGTSCEGGRKVCVSGKCVNCTDKEPATPVHGSNGPAG 550
|:||||:|
212 GLLVCQTHFPWADGTSCEGGRKVCVSGKCVNCTDKEPATPVHGSNGPAG 261

551 PWGDCSRTCCGGGVQYITRECEINPVPRNGGKVCBGRKVRYSNLEDCPEN 600
||||:|
262 PWGDCSRTCCGGGVQYITRECEINPVPRNGGKVCBGRKVRYSNLEDCPEN 311

601 NGKTFREEQCEAHNEFSKASFGNEPTVENTPKYAGVSPDRCKLICAKG 650
||||:|
312 NGKTFREEQCEAHNEFSKASFGSGPAVENTPKYAGVSPDRCKLICAKG 361

651 IGYFFVLQPKVVDGTFCSPDSTSVVCVQGCVCAGCDRIIDSKKQFDKQGV 700
||||:|
362 IGYFFVLQPKVVDGTFCSPDSTSVVCVQGCVCAGCDRIIDSKKQFDKQGV 411

701 CGNGSTCKKMSGIVTSTRPGYHDIITPTGATNDEVKQNRGRSRRNGS 750
||||:|
412 CGNGSTCKKLSGVSITSAPKGYHDIITPTGATNDEVKQNRGRSRRNGS 461

751 FLAIRAADGTYTLNGFTLSTLEBQDLYKGTVLRYSGSSAALERIRSFSP 800
|||:||||:|
462 FLAIRAADGTYTLNGFTLSTLEBQDLYKGTVLRYSGSSAALERIRSFSP 511

801 LKEPLTIQVLNVGHALRPKIDGYTFMROQCTESFNAIPTFSWVTEENGEC 850
||||:|
512 LKEPLTIQVLTVGNALRPKIDGYTFMROQCTESFNAIPTFSWVTEENGEC 560

901 WSPCSKTGGRGYKRTLKCVSHDGGVLSNESCDPLKQPKHYIDFCTLTCQ 950
||||:|
561 ...CSKTGGRGYKRTSLKLSHDGGVLSNESCDPLKQPKHYIDFCTLTCQ 607

951 S* 951
|
608 S* 609

FIG. 6

608 S* 609

gtgcctac	atg	gtc	acg	tcc	ttc	cta	gat	aat	gga	cac	ggg	gaa	tgt	ttg	50	
Met	Val	Thr	Ser	Phe	Leu	Asp	Asn	Gly	His	Gly	Glu	Cys	Leu			
1				5					10							
atg	gac	aag	ccc	cag	aat	cca	atc	aag	ctc	cct	tct	gat	ctt	ccc	ggg	98
Met	Asp	Lys	Pro	Gln	Asn	Pro	Ile	Lys	Leu	Pro	Ser	Asp	Leu	Pro	Gly	
15				20					25					30		
acc	ttg	tac	gat	gcc	aac	cgc	cag	tgt	cag	ttt	aca	ttc	gga	gag	gaa	146
Thr	Leu	Tyr	Asp	Ala	Asn	Arg	Gln	Cys	Gln	Phe	Thr	Phe	Gly	Glu	Glu	
				35				40						45		
tcc	aag	cac	tgc	cct	gat	gca	gcc	agc	aca	tgt	act	acc	ctg	tgg	tgc	194
Ser	Lys	His	Cys	Pro	Asp	Ala	Ala	Ser	Thr	Cys	Thr	Thr	Leu	Trp	Cys	
			50					55					60			
act	ggc	acc	tcc	ggg	ggc	tta	ctg	gtg	tgc	caa	aca	aaa	cac	ttc	cct	242
Thr	Gly	Thr	Ser	Gly	Gly	Leu	Leu	Val	Cys	Gln	Thr	Lys	His	Phe	Pro	
			65				70					75				
tgg	gca	gat	ggc	acc	agc	tgt	gga	gaa	ggg	aag	tgg	tgt	gtc	agt	ggc	290
Trp	Ala	Asp	Gly	Thr	Ser	Cys	Gly	Glu	Gly	Lys	Trp	Cys	Val	Ser	Gly	
	80					85					90					
aag	tgc	gtg	aac	aag	aca	gac	atg	aag	cat	ttt	gct	act	cct	gtt	cat	338
Lys	Cys	Val	Asn	Lys	Thr	Asp	Met	Lys	His	Phe	Ala	Thr	Pro	Val	His	
	95				100					105					110	
gga	agc	tgg	gga	cca	tgg	gga	ccg	tgg	gga	gac	tgc	tca	aga	acc	tgt	386
Gly	Ser	Trp	Gly	Pro	Trp	Gly	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	
				115					120					125		
ggg	ggg	gga	gtt	caa	tac	aca	atg	aga	gaa	tgt	gac	aac	cca	gtc	cca	434
Gly	Gly	Gly	Val	Gln	Tyr	Thr	Met	Arg	Glu	Cys	Asp	Asn	Pro	Val	Pro	
			130					135					140			
aag	aac	gga	ggg	aag	tac	tgt	gaa	ggc	aaa	cga	gtc	cgc	tac	agg	tcc	482
Lys	Asn	Gly	Gly	Lys	Tyr	Cys	Glu	Gly	Lys	Arg	Val	Arg	Tyr	Arg	Ser	
		145					150					155				
tgt	aac	atc	gag	gac	tgt	cca	gac	aat	aac	gga	aaa	acg	ttc	aga	gag	530
Cys	Asn	Ile	Glu	Asp	Cys	Pro	Asp	Asn	Asn	Gly	Lys	Thr	Phe	Arg	Glu	
	160				165						170					
gag	cag	tgc	gag	gcg	cac	aat	gag	ttt	tcc	aaa	gct	tcc	ttt	ggg	aat	578
Glu	Gln	Cys	Glu	Ala	His	Asn	Glu	Phe	Ser	Lys	Ala	Ser	Phe	Gly	Asn	
	175				180					185					190	
gag	ccc	act	gta	gag	tgg	aca	ccc	aag	tac	gcc	ggc	gtc	tgc	cca	aag	626
Glu	Pro	Thr	Val	Glu	Trp	Thr	Pro	Lys	Tyr	Ala	Gly	Val	Ser	Pro	Lys	
				195				200						205		

FIG. 7A

gac agg tgc aag ctc acc tgt gaa gcc aaa ggc att ggc tac ttt ttc	674
Asp Arg Cys Lys Leu Thr Cys Glu Ala Lys Gly Ile Gly Tyr Phe Phe	
210 215 220	
gtc tta cag ccc aag gtt gta gat ggc act ccc tgt agt cca gac tct	722
Val Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser	
225 230 235	
acc tct gtc tgt gtg caa ggg cag tgt gtg aaa gct ggc tgt gat cgc	770
Thr Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg	
240 245 250	
atc ata gac tcc aaa aag aag ttt gat aag tgt ggc gtt tgt gga gga	818
Ile Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly	
255 260 265 270	
aac ggt tcc aca tgc aag aag atg tca gga ata gtc act agt aca aga	866
Asn Gly Ser Thr Cys Lys Lys Met Ser Gly Ile Val Thr Ser Thr Arg	
275 280 285	
cct ggg tat cat gac att gtc aca att cct gct gga gcc acc aac att	914
Pro Gly Tyr His Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile	
290 295 300	
gaa gtg aaa cat cgg aat caa agg ggg tcc aga aac aat ggc agc ttt	962
Glu Val Lys His Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe	
305 310 315	
ctg gct att aga gcc gct gat ggt acc tat att ctg aat gga aac ttc	1010
Leu Ala Ile Arg Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asn Phe	
320 325 330	
act ctg tcc aca cta gag caa gac ctc acc tac aaa ggt act gtc tta	1058
Thr Leu Ser Thr Leu Glu Gln Asp Leu Thr Tyr Lys Gly Thr Val Leu	
335 340 345 350	
agg tac agt ggt tcc tcg gct gcg ctg gaa aga atc cgc agc ttt agt	1106
Arg Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser	
355 360 365	
cca ctc aaa gaa ccc tta acc atc cag gtt ctt atg gta ggc cat gct	1154
Pro Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Met Val Gly His Ala	
370 375 380	
ctc cga ccc aaa att aaa ttc acc tac ttt atg aag aag aag aca gag	1202
Leu Arg Pro Lys Ile Lys Phe Thr Tyr Phe Met Lys Lys Lys Thr Glu	
385 390 395	
tca ttc aac gcc att ccc aca ttt tct gag tgg gtg att gaa gag tgg	1250
Ser Phe Asn Ala Ile Pro Thr Phe Ser Glu Trp Val Ile Glu Glu Trp	
400 405 410	

FIG. 7B

ggg gag tgc tcc aag aca tgc ggc tca ggt tgg cag aga aga gta gtg	1298
Gly Glu Cys Ser Lys Thr Cys Gly Ser Gly Trp Gln Arg Arg Val Val	
115 420 425 430	
cag tgc aga gac att aac gga cac cct gct tcc gaa tgt gca aag gaa	1346
Gln Cys Arg Asp Ile Asn Gly His Pro Ala Ser Glu Cys Ala Lys Glu	
435 440 445	
gtg aag cca gcc agt acc aga cct tgt gca gac ctt cct tgc cca cac	1394
Val Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp Leu Pro Cys Pro His	
450 455 460	
tgg cag gtg ggg gat tgg tca cca tgt tcc aaa act tgc ggg aag ggt	1442
Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly	
465 470 475	
tac aag aag aga acc ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta	1490
Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu	
480 485 490	
tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac	1538
Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp	
495 500 505 510	
ttt tgc aca ctg aca cag tgc agt taagaggcgt tagaggacaa ggtagcgtgg	1592
Phe Cys Thr Leu Thr Gln Cys Ser	
515	
ggaggggctg atacactgag tgcaagagta ctggagggat ccagtgagtc aaaccagtaa	1652
gcagtgaggt gtggcaagga ggtgtgtgta ggggatacat agcaaaggag gtagatcagg	1712
acactaccct gccagttaca ttctgataag gtagttaatg aggcacagta gcatctgaaa	1772
gaccatacag agcactaagg agccccaagg cactattagt atctcttttc ttatatctat	1832
cgcccaata attttcagag tctggcagaa gccctgttgc actgtactaa ctagatactt	1892
cttatcaciaa agattgggaa aggcaaagca gaaagatggg aagactgggt ttcaaacaag	1952
gcttggtttc aatcactgga ggcaaggagg aggggacaaa caagatcatt attcgaagtc	2012
gctggttgct gtggttttac ggaagggtga tgcattcatt ctatcaacag tgaagggttc	2072
agcttggttca acgtgacaga aaggctcatc tccgtgaaag agctcctgat ttcttcttac	2132
accatctcag ttcttaacta tagttcatgt tgaggtagaa acaattcatc tatttataaa	2192
atgtacattg gaaaaaaaaa gtgaagttaa tgaggtagac ataaaaactg aaggaaacaa	2252
tgagcaacat gcctcctgct ttgcttcctc ctgaggtaaa cctgcctggg gattgaggtt	2312
gtttaagatt atccatggct cacaagaggc agtaaaataa tacatgttgt gccagagtta	2372
gaatggggta tagagatcag ggtcccatga gatggggaac atggtgatca ctcatctcac	2432
atggggaggct gctgcagggg agcagggtcca ctctggcag ctgggtccaa agtcgtatcc	2492
tggtgaatgt ctgttcagct cttctactga gagagaatat gactgtttcc atatgtatat	2552
gtatatagta aaatatgtta ctatgaattg catgtacttt ataagtattg gtgtgtctgt	2612
tccttctaag aaggactata gtttataata aatgcctata ataacatatt tatttttata	2672
cattttatttc taatgataaa acctttaagt tatatcgctt ttgtaaaagt gcatataaaa	2732
atagagtatt tatacaatat atgttaacta gaaataataa aagaacactt ttgaatgtgt	2792
atgcctatct tctggagtgg gattaacttc tgggcaagaa atctgatgag acacaaacat	2852
tggacttcaa gacagtttta aattttgggt aaatgaactg tatttcctgt ttatagacgt	2912
actaataaaa aagaagtga tgatgtcttt agtggttaaga ttgttactaa tgtgggtggc	2972
aaattgctgt aaagagccag atagtaagca tttatggcat tgtaggctat ctttctgcc	3032
acaaccatgt gacagtgagt gctttgtagg actgagagca gccataaatg acatgtaaat	3092
gataaactgt ggctgtgctt taataaaaact ttatttacaa aaaaaaaaaa aaa	3145

FIG. 7C

gcggccgctc ccggccggcc caagggacag agccaggctc cgggagcccg caacactcgt	60
cctgagagcc ccggctcctc agcccgcctac ggccagggcc tcggcctccg cccccgactc	120
ccgagctcct gccctagagt cgactyggct cccgcccgcg tgggacagac agacggacag	180
ccagccctgc gagggcgcg gcaccgggcg gaggtgttgt aggaggagac cgaggagggg	240
ggctgggctg gggctggggc cgcgccggca agagagacat gcgattggtg accaagccga	300
gcggacggac agcgcgccc ag atg cag gtg agc gag agg atg ctg gca ggg	352
Met Gln Val Ser Glu Arg Met Leu Ala Gly	
1 5 10	
ggg atg aga agc atg ccc agc ccc ctc ctg gcc tgc tgg cag ccc atc	400
Gly Met Arg Ser Met Pro Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile	
15 20 25	
ctc ctg ctg gta ctg ggc tca gtg ctg tca ggc tct gct aca ggc tgc	448
Leu Leu Leu Val Leu Gly Ser Val Leu Ser Gly Ser Ala Thr Gly Cys	
30 35 40	
ccg ccc cgc tgc gag tgc tca gcg cag gac cga gcc gtg ctc tgc cac	496
Pro Pro Arg Cys Glu Cys Ser Ala Gln Asp Arg Ala Val Leu Cys His	
45 50 55	
cgc aaa cgc ttt gtg gcg gtg ccc gag ggc atc ccc acc gag act cgc	544
Arg Lys Arg Phe Val Ala Val Pro Glu Gly Ile Pro Thr Glu Thr Arg	
60 65 70	
ctg ctg gac ctg ggc aaa aac cgc atc aag aca ctc aac cag gac gag	592
Leu Leu Asp Leu Gly Lys Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu	
75 80 85 90	
ttt gcc agc ttc cca cac ctg gag gag cta gaa ctc aat gaa aac atc	640
Phe Ala Ser Phe Pro His Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile	
95 100 105	
gtg agc gcc gtg gag cca ggc gcc ttc aac aac ctc ttc aac ctg agg	688
Val Ser Ala Val Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg	
110 115 120	
act ctg ggg ctg cgc agc aac cgc ctg aag ctt atc ccg ctg ggc gtc	736
Thr Leu Gly Leu Arg Ser Asn Arg Leu Lys Leu Ile Pro Leu Gly Val	
125 130 135	
ttc acc ggc ctc agc aac ttg acc aag ctg gac atc agt gag aac aag	784
Phe Thr Gly Leu Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys	
140 145 150	
atc gtc atc ctg cta gac tac atg ttc caa gac cta tac aac ctc aag	832
Ile Val Ile Leu Leu Asp Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys	
155 160 165 170	
tcg ctg gag gtc ggc gac aac gac ctc gtc tac atc tcc cat cga gcc	880
Ser Leu Glu Val Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala	
175 180 185	

FIG. 8A

ttc agc ggc ctc aac agc ctg gaa cag ctg acg ctg gag aaa tgc aat	928
Phe Ser Gly Leu Asn Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn	
190 195 200	
ctg acc tcc atc ccc acg gag gcg ctc tcc cac ctg cac ggc ctc atc	976
Leu Thr Ser Ile Pro Thr Glu Ala Leu Ser His Leu His Gly Leu Ile	
205 210 215	
gtc ctg cgg cta cga cat ctc aac atc aat gcc atc agg gac tac tcc	1024
Val Leu Arg Leu Arg His Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser	
220 225 230	
ttc aag agg ctg tac cga ctt aag gtc tta gag atc tcc cac tgg ccc	1072
Phe Lys Arg Leu Tyr Arg Leu Lys Val Leu Glu Ile Ser His Trp Pro	
235 240 245 250	
tac ctg gac acc ata acc ccc cgg acg cgt ggg tcg ac	1110
Tyr Leu Asp Thr Ile Thr Pro Arg Thr Arg Gly Ser	
255 260	

FIG. 8B

ctcctggatg tgcgcagccg cagagcgctg ctgctgtgcc taatacccat cgctgcgcac 60
 ttgacagcca gtccgcccggt ccggagcccg gctcgttggg gcagc atg gcg ggg tgc 117
 Met Ala Gly Ser
 1

ccg ctg ctc tgc ggg ccg cgg gcc ggg ggc gtc ggc att ttg gtg ctg 165
 Pro Leu Leu Cys Gly Pro Arg Ala Gly Gly Val Gly Ile Leu Val Leu
 5 10 15 20

ctg ctc ttg ggc ctt ctg agg ctg ccc ccc acc ctg tca gcg agg ccc 213
 Leu Leu Leu Gly Leu Leu Arg Leu Pro Pro Thr Leu Ser Ala Arg Pro
 25 30 35

gtg aag gag ccc cgc agt ctg agc gca gca tcc gcg ccc ttg gtt gag 261
 Val Lys Glu Pro Arg Ser Leu Ser Ala Ala Ser Ala Pro Leu Val Glu
 40 45 50

acg agc act ccc ctc cgc ttg cgt cgg gcc gtg ccc cga gga gag gcg 309
 Thr Ser Thr Pro Leu Arg Leu Arg Arg Ala Val Pro Arg Gly Glu Ala
 55 60 65

gcg ggt gcg gtg cag gag ctg gcg cgg gcg ctg gcg cac ctg ctg gag 357
 Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu Leu Glu
 70 75 80

gcc gag aga cag gaa cgc gcg cgt gct gag gcg cag gag gct gag gat 405
 Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala Glu Asp
 85 90 95 100

cag cag gcg cgt gtc ctg gcg cag ctg ctg cgc gcc tgg ggc tct ccg 453
 Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Ala Trp Gly Ser Pro
 105 110 115

cgt gcc tcg gac ccg ccc ttg gcc ccc gac gat gac ccg gac gct cca 501
 Arg Ala Ser Asp Pro Pro Leu Ala Pro Asp Asp Asp Pro Asp Ala Pro
 120 125 130

gct gca cag ctc gcc cgt gct ctg ctc cga gct cgc cta gac ccc ggc 549
 Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp Pro Gly
 135 140 145

ccc cag tgt atg atg atg gcc cca ctg gcc cag acg tcg agg atg ccg 597
 Pro Gln Cys Met Met Met Ala Pro Leu Ala Gln Thr Ser Arg Met Pro
 150 155 160

gcg acg aga ctc ctg acg tgg acc ctg agc tgc tgaggtactt gctagggcgg 650
 Ala Thr Arg Leu Leu Thr Trp Thr Leu Ser Cys
 165 170 175

atcctcaccg gaagtccgga gccagaggct gctcctgccc cgcgccgcct ccgccgatct 710
 gtggaccagg atttgggtcc cgaggtgccc cctgagaacg tactgggggc tctgctacgc 770
 gtcaaacgcc tggagaaccc ctgcgccag gcgccggcac gccgcctcct gcctccctga 830

FIG. 9A

gcggtgctgc atcctgcacg ccctggaacc caggagcgcc ccagcaaccc tgactccctg 890
 ccagcacgtc caaggctgct taccacagca acctcccatc ccctgagccc tcaataaatg 950
 ccatctgtag caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1010
 aaaaaaaaaa aaaaaaa 1027

FIG. 9B

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